GenCore version 5.1.3 Compared its

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OM nucleic - nucleic search, using sw model
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1: /SIDS2/ary3a14/a/a
2: /SIDS2/ary3a14/a/a
2: /SIDS2/ary3a14/a/a
4: /SIDS2/ary3a144/a/a
5: /SIDS2/ary4a14/a/a
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1 gigelolaatettitetggtaceagg 26
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Listing first 45 summaries
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/SIDS2/grgdata/geneseg/genesegn-embi/NA1986-DAT:*
/SIDS2/grgdata/geneseg/genesegn-embi/NA198-DAT:*
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/SIDS2/gcgddata/geneseq/geneseqn-embl/MA2001A.DAT:
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11055.609 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result.		Query				
No.	SCCIT	Matich	Match bength DB		10	Desertption
-	26	100.0	26	24	АНІ.57124	Cattle growth horm
2	56	100.0	in to	13	ABL57128	Cattle growth horm
¥	25	100.0	540	24	ABL57127	Cattle growth horm
4	ນ	100.0	2869	14	ABL57126	Cattle growth horm
a 5	18.2	70.0	1236	i)	AAS00247	Bcl-Xl-DTR apoptos
c 6	18.2	70.0	1608	.1 8	AAV05129	DNA encoding dipth
c 7	18.2	70.0	1704	22	AAS00248	Bad-DTTR apoptosis
ი 8	18.2	70 O	10,1	.n	AA2=4349	Dightheria toxio (
c 9	16.2	70 0	1933	17.5	AAQ5433B	Diphtheria toxin d
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ALIGNMENTS

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Obtaining head of beef sattle with genetic predisposition for altered carcass weight, by assaying genetic material from head for polymorphism	WF1; 2002-417707/45.			Lucy MC, Lubahn DB, Keisler DH, Shibuya H, Johnson GS, Herring WO:		(UMOR) UNIV MISSOURI.		20-JUL-2000; 2000CA-2312269.		20-JUL-2000; 10000A:1312269.		20-JAN-2002.		CA2312269-A1.		Bos taurus.		midtusatellite, marker-assisted selection; PCR; primer; ss.	Cattle, beef, breeding, growth hormone, somatotropin, receptor;		Cattle growth hormone receptor gene TO-repeat T' FOE primer.	orace lee (tire entry)		ARLS/184;		RESULT 1 ABL57124 ID ABL57124 standard: DNA; 26 BP.

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RESULT 2
ABL57128
XX
AC ABL57
XX
DT 05-A
DT 05-A
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Best Local :
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20-101 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cattle; beef; breeding; growth hormone; somatotropin; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cattle growth hormone receptor gene premoter and even la region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compared with cattle having fewer than 12 copies of the TG dinucleotide repeat. Use of this marker and other genetic markers in linkage disequilibrium with the locus allows implementation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a primer that corresponds to nucleotides located 5 to a polymorphic TG repeat microsatellite located 90 bp upstream from a major transcription start site in the bowine growth hormone receptor gene (see AH157124). The TG-repeat microsatellite can be used as a genetic marker that correlates with cattle growth cattle having at least 12, and preferably 16-20, copies of the TG dinucleutide repeat marker show increased carcass or meaning weight
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                                                           26 JUL 2000; 2000CA-2312269
                                                                                                                         20 JAN 2002.
                                                                                                                                                                                                                                                                                                                                                                                                             variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selection and breeding schemes for improvement of cattle performance. Marker resisted selection with the jenetic markets avoids the costly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AHI.57128 standard; DNA; 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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2000CA 2312269
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replace(473,6)
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275..300
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ABL57127
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Bost Local S
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with the locus allows implementation. Other denetic schemes for improvement of cattle performance. Other denetic markers may include polymorphisms such as the G/A polymorphic estre in exon IA. The A allele (found in indicine cattle) contains a Draf restriction site that is not present in the G allele (found in taurine cattle). This difference can be used in a PCR/RFLP in taurine cattle). This difference can be used in a PCR/RFLP in taurine cattle).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in taurine cattle). This difference can be used in a PCK/RFLP assay to distinguish the respective alicies. The 2 Dz. upstream polymorphic sites could similarly be used. Marker assisted selection with the genetic markers avoids the costry phenotypic testing associated with traditional breeding schemes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and carcass weight of cattle. Cattle having at least 12, and preferably 16-20, explos of the TC dinneleptide repeat marker show increased carcass or weaning weight compared with cattle having fewer than 12 copies of the TC dinnelected the repeat. Use this marker and other genetic markers in linkage disequilibrium with the locus allows implementation of selection and breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hale CS;
                   exon
                                                                                                                         satellite
                                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                    Cattle growth hormone receptor gene promoter and exon 1A region
                                                                                                                                                                                                                                                                                                                                                                              05-AUG-2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL57127 standard; DNA; 540 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bottome growth hormone teceptor gene. A perghorphic TG-repeat migrosatellite located 90 bp upstream from a major transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obtaining head of beef cattle with genetic predisposition for altered catcass weight, by assaying genetic material from head for polymorphism linked to promoter Pl of exon IA of bovine growth hormone receptor gene
                                                                                                                                                                 primer_bind
                                                                                                                                                                                                                                                                        microsatellite, marker assisted Selection, ds
                                                                                                                                                                                                                                                                                            Cattle; beef; breeding; growth hormone; somatotropin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 522 BP; 124 A; 121 C; 136 G; 141 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UMOR ) UNIV MISSOURI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 GTGCTCTAATCTTTTCTGGTACCACG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIGCICTAATCITTTCTGGTACCAGG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 100.0%; Score 26; D8 24; Length 522;
Similarity 100.0%; Pred. No. 0.034;
26; Conservative 0, Mismatches 0, Indels
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             /*tag- c
362..540
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/mote- "TG dimodeotide repeat microsatellite"
                                                                                                                                        /*tag-
                                                                                                                                                              complement (207..232)
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/*tag- d
                                                           293..318
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variation

febiace(12,T)

/number- lA

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ABL57126
ID ABL5
XX
AC ABL5
XX
AC C5-J
DT 05-J
XX
DE Catt
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Catt
                                                                                                                                                                                                        RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assay to distinguish the respective alleles. The 2 1/2 upstream polymorphic sites could similarly be used. Marker-assisted selection with the genetic markers avoids the costly phenotypic resting associated with traditional breeding schemes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with the marker and other genetic markers in linkage disequilibrium with the locus allows implementation of selection and breeding schemes for improvement of cattle performance. Other genetic markers may include polymorphisms such as the G/A polymorphic site in exon IA. The A allele (found in indictine cattle) contains a Drai restriction site that is not present in the G allele (found in taurine cattle). This difference can be used in a PCR/RFID assay to distinguish the respective alleles. The 2 i/C upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bovine growth humane receptor year. A polymorphic TG repeat microsatellite located 90 bp upstream from a major transcription start site in the gene is associated with average weaning weight and carcass weight of cattle. Cattle having at least 12, and preferably 16-20, copies of the TG dinucleotide repeat marker show increased carcass or weaning weight compared with cattle having fewer than 12 copies of the TG dinucleotide repeat. Use child the total cattle having fewer than 12 copies of the TG dinucleotide repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA2312269 A1
Cattle; beef; breeding; growth hormone; somatotropin; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obtaining head of beef cattle with genetic predisposition for altered carcass weight, by assaying genetic material from head for polymorphism linked to promoter PI of exon IA of bovine growth hormone receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variation
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 540 BP; 123 A; 123 C; 146 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2: Fig 3; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFI, 2002 417707,'45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-2000; 2000CA-2312269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variation
                                    Cattle growth hormone receptor gene promoter and exon 1A region
                                                                                 05-AUC-2002
                                                                                                                        ABL57126;
                                                                                                                                                                 ABI.57126 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the promoter and exon 1A region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hale CS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lucy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UMOR ) UNIV MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-2000; 2000CA-2312269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JAN-2002
                                                                                                                                                                                                                                                                    207 GEGCECTAATCTTTTCTGGTACCAGG 232
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                          1 GTGCTCTAATCTTTTCTGGTACCAGG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lubahn DB,
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace(491,A)
/*tag==g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replace(94,T)
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*Laq- e
/standard_name- "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        />tundard_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name=
                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 26; DB 24; 100.0%; Pred No 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keisler DH,
                                                                                                                                                                 2869 BP
                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Single mucleutide pulymurphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibuya H, Johnson GS,
                                                                                                                                                                                                                                                                                                                                                  ço
                                                                                                                                                                                                                                                                                                                                                                                        Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herring WO;
                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                Gaps
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SEXEXE SEX EX
                                                                                                                                                                                                                                            Db
                                                                                                                                                             AAS00247/c
                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lucy MC,
Hale CS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microsatellite; marker-assisted selection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    show increased carcass or weaning weight compared with cattle having fewer than 12 copies of the TG dinucleotide repeat. Use this marker and other genetic markers in linkage disequilibrium with the locus allows implementation of selection and breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      start site in the gene is associated with average weaning weight and carcass weight of cattle. Cattle having at least 12, and preferably 16-20. copies of the TG dimensional description marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bovine growth hormone receptor gene. A polymorphic 13-repeat microsatellite located 90 bp upstroam from a major transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obtaining head of beef cattle with genetic predisposition for altered carcass weight, by assaying genetic material from head for polymorphism linked to promoter Pi of exon IA of bovine growth hormone receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA2312269-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            satellite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200
                                                     31-MAY-2001 (first entry)
                                                                                                                                                                                                                                            2580 GIGCICIAAICTITICIGGIACCAGG 2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  schemes for improvement of cattle performance. Marker-assisted selection with the genetic markers avoids the costly phenotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 41-43; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-417707/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer_bind
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          Bcl-Xl-DTR apoptosis-modifying fusion protein, DNA sequence
                                                                                                AAS00247
                                                                                                                                         AAS00247 standard; DNA; 1236
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2869 HP; 657 A; 640 C; 582 G; 990 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              testing associated with traditional breeding schemes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          boviñe growth hormone receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the promoter and exon 1A region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UMGR ) UNIV MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 Jul. 2000, 2000CA-2312269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-2000; 2000CA-2312269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JAN-2002
                                                                                                                                                                                  J
                                                                                                                                                                                                                                                                                 1 GTGCTCTAATCTTTTCTGGTACCAGG 26
                                                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lubahn DB,
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*t.ag= c
2735..2869
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag-
2507...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (2580..2605)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2666..2680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number- 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                             100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 2646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keisler DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               § dimueleutide repeat microsatellite"
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                             Score 26; DB 24
Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibuya H,
                                                                                                                                                                                                                                                                                                                                                               DB 24;
                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johnson GS,
                                                                                                                                                                                                                                                                                                                                                                 Length 2869;
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Herring WO.

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(inhibiting or enhancing) apoptosis in a target cell, such as neuron, lymphocyte, cureer, reoplasm, macrophage, epithelial, stem, timour explayment if craftice cell or an adjooryte. It is also useful for reducing apoptosis in a subject after transient ischaemic neuronal injury, capetially spital cord injury. The fusion protein may be used to treat carriers discasses and injury conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alcheimed's discase. Heatington's discass. Spital mescalar
                                                                                                                                                                                                                                                                                                                                                                                                                target cell and integrating into or crossing a cellular membrane of the target cell. The apoptosis modifying fusion protein comprises at least two domains: the DFR domain, which hargets the fusion protein to the target cell and the Bel-XL domain, which modifies an apoptotic response of the target cell. The tusion protein is useful for modifying of the target cell.
atrophy, struke episodes and unregulated cell growth as in tumours and various cancers. The apoptosis modifying fusion protein can be delivered officelyvely throughout the body and targeted to selective fissue and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents the coding sequence of BeT-XI-DTR apoptosis-modifying fusion protein comprising human BeT-XI sequence fused via a short linker to diphtheria towin receptor binding domain (DTB). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mise_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           functional apoptosis-modifying fusion protein is capable of binding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 54:56; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Youle RJ, Liu X, Collier RJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD CULLEGGE.
(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 AUG 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 AUG 2000; 2000WO-US2229+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 FEB 2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimer is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200112661-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium diptheriae
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/mode- "Linker DNA, linking Rel-XI to DTP"
778..1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag== b
Znote== *16x Histidine tag
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/mote- "DTR, diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              760.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "DTR is diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag==a
/product=="Bel-Xl-DTR lusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*1 aq-
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Matches 20; Query Match Bust Local Similarity

Conservative

0; Mismatches Score 18.2; 58 18; Pred. No. 1.3c+02;

Indels

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Gaps

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:cngth 1608;

70.0%; 87.0%;

sequence 1608 BP; 492 A; 294 t; 382 G; 440 T; 0 other;

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                                                  The present sequence encodes a diphtheria toxin. Regions of the present sequence can be utilised as broad range helper I cell epitopes in DNA plasmid based vaccines against cholesteryl ester transfer proteins (CETPs). CETPs mediate the transfer of cholesteryl esters from high density hipoprotein (HDL), to very low density hipoprotein (VDD) and vice versa. An increased CETP activity produces an atherosclerosis. A DNA plasmid-based vaccine comprises sequences encoding at least one B cell epitope of CETF linked in frame with at least one segment encoding a broad range helper I cell epitope. The vaccines can be used to elevate the ratio of circulating HDL to circulating HDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1188 GTGATCTACTGTTTTCTGGTACC 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1236 BF, 317 A, 291 C, 345 C, 285 T; O other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENA plasmid based vaccine encodes CETP B cell and helper T cell epitope(s) - used for elevating high density lipoprofein levels, for treating cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    high density lipoprotein; HDL; very low density lipoprotein; VLDL; Toell epitope; antibody; DNA plasmid-based vaccine; broad range helper Toell epitope;
                            anti-CETF antibodies in vivo and for treating cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Pages 40-42; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW46448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-549731/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TCEL-) T CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 · FEB · 1997;
01 · MAY · 1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09741227-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment; cardiovascular disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cholesteryl ester transfer protein, CETP; cholesteryl ester;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding diptheria toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV05129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV05129 standard; cDNA; 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conscruative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1236;
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AAS00248/c
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                                                                    target cell. The apoptosis-modifying fusion protein comprises at least two domains: the DTR domain, which targets the Jusion protein to the target cell and the Bcl XL domain, which modifies an apoptosic response of the target cell. The fusion protein is useful for modifying finhibiting or enhancing) apoptosis in a target cell, such as neuron, lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-proliferative cell or an adipocyte. It is also useful for reducing
               apoptosis in a subject after transient ischaemic neuronal injury, especially spinal cord injury. The fusion protein may be used to treat various diseases and injury conditions through inhibition or enhancement
                                                                                                                                                                                                                                       The sequence represents the coding sequence of Bad-DTTR apoptosis modifying tusion protein comprising Bad gene sequence fused via a linker to diphtheria toxin translocation domain (DTTR). The
                                                                                                                                                                                                                                                                                                                                                                       Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diphtheria toxin receptor binding domain; DTTR; neoplasm; tumour; hyper proliferation, Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1560
                                                                                                                                                                                                    functional apoptosis-modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the
                                                                                                                                                                                                                                                                                                                  Claim 5; Page 57-59; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W0200112661-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huntington's disease, diphtheria toxin translocation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bad-DTTR apoptosis-modifying fusion protein, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2001
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of apoptotic cellular response, including neurodegenerative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAU00220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCTCTAATCTTTTCTCCTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-218343/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAPVARD COLLECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu X, Collier RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium diptheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9905-0149220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "DTTR is diphtheria toxin translocation domain" 7..36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualitiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Bad-DTTR fusion protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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                        Oligonucleotide directed mutagenesis of the wild-type diphtheria grame (specifically the region encoding the TR A fragment) results in describe of the codons for Val 147 and active site residues. The resulting muteins are not toxic, making them useful in diphtheria vaccines. The risk of reversion to toxicity is muto lower for the 147-148 double mutants than for the prior art 148 single mutant, while their immunogenicity is not impaired. The specification while their immunogenicity is not impaired. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as Alzheimer's disease, Buntington's disease, spinal muscular atrophy, stroke episodes and unregulated evil growth as in tumours and various cancers. The appricasis modifying fusion protein can be delivered effectively throughout the body and targeted to selective tissue and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1656 GTGATCTACTGTTTTCTGGTACC 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DT; protein exotoxin: NAD-dependent ADP-ribosyltransferase; vaccine diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ54340 standarg; DNA; 1921 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1704 BP; 470 A; 395 C; 444 G; 395 T; 0 other;
                                                                                                                                                                              Claim 4; ; 42pp; English.
                                                                                                                                                                                                                            New DNA encoding diphtheria toxin deletion mutants - with toxicity and low risk of reversion, and derived toxoids ar
                                                                                                                                                                                                                                                                                P-PSDB; AAR44892
                                                                                                                                                                                                                                                                                                                                 Collier PJ,
                                                                                                                                                                                                                                                                                                                                                                (HAPD ) HAPVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diphtheria toxin (delta-142 to 148) mutant coding sequence
                                                                                                                                                                                                              transformed cells, useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09325210-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reversion mutation; site-directed mutagenesis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1994 (first entry)
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                                                                                                                                                                                                                                                                                                1994-007178/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                 Killeen K,
                                                                                                                                                                                                                                                                                                                                                                                                 92US-0901712
                                                                                                                                                                                                                                                                                                                                                                                                                                   93WO-US04606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= delta-142_to_-148_diphtheria_toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312..1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "single chain translation product is readily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag-
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87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to 148 have been deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cleaved to form two subunits (A and B). In by a disulphide bond; wild-type codons 142
                                                                                                                                                                                                                                                                                                                                 Mekalanos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.2;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1704;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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includes the wild-type DT coding sequence but does not include any

sequences; the wild-type sequence was modified

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Bost Local Similarity 87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                      oligonucleotide directed mutagenesis of the wild-type diphtheria gene (specifically the region encoding the PrA fragment) results in detertion of the codons for Val-147 and active site residue (In 148 and opt. deletion or substitution of other active residues. The resulting mutains are not toxic making them useful to diphtheria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the description in the claims to give AAQ54340.
                                                                                                                                 tractions. The stabled services in the prior art 148 shall sweet by the 147 148 doubte motants than for the prior art 148 shale metant, while their communication is not impaired. The specification includes the wild type DT coding sequence but does not include any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1850 GTGATCTACTGTTTTCTGGTACC 1828
Sequence 1933 BP; 574 A; 359 C; 468 C; 533 T; 0 other;
                                                              mutant sequences; the wild type sequence was modified according to the description in the claims to give AAQ5438.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ54338 standard; DNA; 1933 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; ; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transformed cells, useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxicity and low risk of reversion, and derived toxoids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA encoding diphtheria toxin deletion mutants - with no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARO ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TH JUN 1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 MAY 1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reversion mutation, site directed matagenesis, do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diphtheria toxeid; deletion mutant; mutein; variant; double mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE: protein exotoxin; NAD dependent ADP-ribesyltransferms; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 JUN 1994 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Killeen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2151050-5075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93WO US04606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product - delta 142 147 148_diphtheria_toxin
/note- "simple chain translation product is readily
/note- "simple chain translation product is readily
cleaved to form two subunits (A and B), linked
by a disulphide bond; wild type codons 142
(Glu), 147(Val) and 148(Glu) have been detected"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*t aq-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112..1910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the state of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mekalanos J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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AAQ54337/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outry Match
Host Local Similarity 87.0
Matches 20, Concernative
          while their immunogenicity is not impaired. The specification includes the wild type DT coding sequence hat does not include any metant sequences. The wild type sequence was modified according to
                                                                 The resulting materias are not toxic, making them useful in diphtheria vaccines. The risk of reversion to toxicity is much lower for the 147-148 double mutants than for the prior art 148 single mutant,
                                                                                                                  uene (specifically the region encoding the DT-A tragment) results in deletion of the codons for Val-147 and active site residue slu-148 and opt, deletion or substitution of other active residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DT: protein exotoxin; NAD-dependent ADP:ribosyltransferase; vaccine; diphtheria toxoid; deletion mutant; mutein; variant; double mutant; reversion mutation; site-directed mutagenesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ54337 standard; DNA; 1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1862 GEGATCTACTGTTTTCTGGTACC 1840
the description in the claims to give AAO54337.
                                                                                                                                                                     Oligonucleotide-directed mutagenesis of the wild-type diphtheria
                                                                                                                                                                                                        Claim 1: : 42pp: English.
                                                                                                                                                                                                                                            transformed cells, useful in vaccines
                                                                                                                                                                                                                                                           New DNA encoding diphtheria toxin deletion mutants—with no toxicity and low risk of reversion, and derived toxids and
                                                                                                                                                                                                                                                                                                                 PEPSDH; AAR44889
                                                                                                                                                                                                                                                                                                                                                                  Collier RJ, Killeen K,
                                                                                                                                                                                                                                                                                                                                                                                                   (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9325210-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diphtheria toxin delta-147-148 mutant coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA054337
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                                                                                                                                                                                                                                                                                                                                1994-007178/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                      9208-0901712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-US04606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product- delta:147:148_diphtheria_toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 noration/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*! aq-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sight have transfat to point as reali-
cleaved to form two subunits (A and B), Hi
by a disniphide bend; wild-type codons 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Val) and 148(Glu) have been deleted"
                                                                                                                                                                                                                                                                                                                                                                  Mekalahas J:

    Mismal thes

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Pred. No. 1.3e(02);
n. Mismatches 3;
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Query Match 70.0%; Best Local Similarity 87.0%;

Sequence 1936 BP; 574 A; 359 C; 470 G; 533 T; 0 other;

Matches

Conservative

0, Mismatches

Indels Length 1936;

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Gaps

<u>.</u>

Score 18.2; DB 15; Pred. No. 1.3e+02;

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RESULT 11
AAQ54339/c
IDAQ5433
XX AAQ5433
XX AAQ543
XX AAQ543
XX AAQ543
XX D1phth
XX DT; pr
KW DT; pr
KW Coryne
FT KW FT CDS
FT C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference 735..737
                                                                                                                               The resulting mateins are not toxic, making them useful in diphtheria vaccines. The risk of reversion to toxicity is much lower for the 147-148 double mutants than for the prior art 148 single mutant, while their immunogenicity is not impaired. The specification includes the wild-type of ceding sequence but does not include any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collier RJ, Killeen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09325210-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diphtheria toxoid; deletion mutant, mutein, variant, double mutant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diphtheria toxin (delta-147-148; E142X) mutant coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ54339 standard; DNA; 1936 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1865 GTGATCTACTGTTTTCTGGTACC 1843
   Sequence 1936 HP; 573 A; 359 C; 468 C; 533 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide-directed mutagenesis of the wild-type diphtheria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transformed cells, useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding diphtheria toxin deletion mutants - with no toxicity and low risk of reversion, and derived toxicids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR44891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-1994
                                                                                                      mutant sequences; the wild-type sequence was modified according to
                                                                                                                                                                                                                                                                                                 Glu-148 and opt. deletion or substitution of other active residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reversion mutation; site-directed mutagenesis; ds.
                                                               the description in the claims to give AAO54339
                                                                                                                                                                                                                                                                                                                                     gene (specifically the region enceding the STA fragment) results in deletion of the godens for Val 147 and active site residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTGCTCTAATCTTTTCTGGTACC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein exotoxin, NAD dependent ADF ribosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1994-007178/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0901712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93WO-US04606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "single chain translation product is readily cleaved to form two subunits (A and B), lin by a disulphide bond; wild type codons 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product- delta 147 148,E142X_diphtheria_toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311..1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "wild-type GAG (Glu) rodon substd by rodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*taq-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142(Glu) has been altered"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Val) and 148(Glu) have been deleted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for any other amino acid*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mekalanos J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine
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Matches

20;

Conservative

0;

Local Similarity

70.0%; 87.0%;

Score 18.2; DB 15; Pred. No. 1.3e+02; Mismatches

1.3e+02;

Length 1936; Indels

0.

Gaps

0,

Sequence 1936 BP;

573 A; 357 C; 470 G; 533 T; 3 other;

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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                          different amino acid residue. The third residue can be in the fragment A (see AAQ54341-7) or in the fragment B (see AAQ54348-054350) portion of DT. The resulting muterins are not toxic, making them useful in diphtheria vaccines. The risk of neversion to toxicity is much lower for the 147-148 double mutants than for the prior art 148 single include. While their immunopericity is not implaired. The specification includes the wild-type DT coding sequence but does not include any mutant sequences; the wild-type sequence was modified according to the description in the claims to give AAQ54341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DT, protein exotoxin, NAC dependent ANN'nibosyltransferase, vaccine diphtheria toxoid; deletion mutant; mutein; variant; double mutant; reversion mutation; site-directed mutagenesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ54341 standard; DNA; 1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1865 GTGATCTACTGTTTTCTGGTACC 1843
                                                                                                                                                                                          Oligonuclectide directed mutagenesis of the wild-type diphtheria gaze results in deletion of the codons for Val-147 and active site residue which is essential for the full toxic activity of wild type DT is deleted or altered to encode a toxic activity of wild type DT is deleted or altered to encode a
                                                                                                                                                                                                                                                                                  Claim 7; ; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09325210-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_difference 372..374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diphtheria toxin (delta-147-148; H21X) mutant coding sequence
                                                                                                                                                                                                                                                                                                                                       New DNA encoding diphtheria toxin deletion mutants - with no toxicity and low risk of reversion, and derived toxoids and
                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR44893
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collier RJ, Killeen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1994
                                                                                                                                                                                                                                                                                                                        transformed cells, useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 1994-007178/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BARD ) HARVARD COLLEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-US04606.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "wild-type CAC (His) codon is replaced by
codon for any other amino acid or is absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= diphtheria_toxin_mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,∕*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Single chain translation product is readily cleaved to form two subunits (A and B), lib by a disulphide bond; wild type codons 147 (Val) and 148(Glu) have been deleted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the His(21) codon is altered or deleted*
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mekalanos J;
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AAQ54342/c
115 AAQ54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall Offices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Ideal Similarity
            portion of DT. The resulting materins are not toxic, making them useful in diphtheria -various. The risk of reservice to taxlety is much lower for the 147-148 double mutants than for the prior art 148 single mutant, while their immunoscenicity is not impaired, the specification
                                                                             residue du 148; opt, a third residue which is essential for the full toxic petiglity of wild type DS is deleted or altered to encode a different amino acid residue. The third residue can be in the tragment A (see AAOS4341 7) or in the tragment B (see AAOS4348-OS4358)
                                                                                                                                             oligonucleotide directed mutagenesis of the wild-type diphtheria gene results in deletion of the codema for Val-147 and active site
                                                                                                                                                                                                                                             New DNA encoding diphtheria toxin deletion mutants - with no toxicity and low risk of reperting, and derived textids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mise ditterence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DF; protein excitoxin; NAU dependent ANF ribusyltransferase; vaevino, diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU54342 standard; DNA; 1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1865 Grearchacherreregrade 1843
                                                                                                                                                                                               Claim 7; ; 42pp; English
                                                                                                                                                                                                                                 transformed cells, useful in
                                                                                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                 TB JUN 1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                17 MAY 1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 DEC. 1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO3325210 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reversion autation; sile directed autagenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diphtheria toxin (delta 147-148; G22X) mutant coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 JUN 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ54342
includes the wild type of coding sequence but does not include any
                                                                                                                                                                                                                                                                                                   P PSDB; AAR44894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1994 007178/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ('onservative
                                                                                                                                                                                                                                                                                                                                                 Killeen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (limit entry)
                                                                                                                                                                                                                                                                                                                                                                                                                9208 0901712
                                                                                                                                                                                                                                                                                                                                                                                                                                                9 1WO US04606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - ht 1*/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.0%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "wild type ord (Cly) solution replaced by codon for any other amino acid or is absent N.B. the amino acid at position 22 of the wild-type by is given as Glu in the claims."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "single chain translation product is readily cleaved to form two subunits (A and B), limby a disulphide bond, wild type codons 147 (Val) and 148(Glu) have been deleted and the Gly(22) rodon is altered or deleted."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ء
                                                                                                                                                                                                                                                                                                                                                 Mekalanos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diphtheria_toxin_mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.2; DB [5; Length 1936; Proof. No. 1.30:02;
                                                                                                                                                                                                                                   vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inked
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THE PROPERTY OF A STANFORD THE PROPERTY OF A STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1865 GEGATOTAGEGETTTOTGGEAGC 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutant sequences, the Wild type sequence was modified according to the description in the claims to give AAOS4342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collier RJ, Killeen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ54343 standard; DNA; 1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1936 BP; 574 A; 359 C; 467 G; 534 T; 3 other;
                                                             different anims weld residue. The third residue can be in the tragment A (see AAQ54341-7) or in the tragment B (see AAQ54348-Q54350)
                                                                                                                                  residue Glu 148; opt. a third residue which is essential for the full toxic activity of wild type DT is deleted or altered to encode a
                                                                                                                                                                                                       Obligational coulded directed mutagenesis of the wild type diphtheria gene results in deletion of the codons for Val-147 and active site
                                                                                                                                                                                                                                                                                                                Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                    transformed cells, useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New BNA encoding diphtheria toxin deletion mutants - with no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9325210-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            miss_difference 426..428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conjudanteriam diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reversion mutation; site directed mutagenesis, ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D); protein exotoxin; NAD-dependent ADP-ribosyltransferase;
diphtheria toxold; deletion matant; mutein; variant; double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diphtheria toxin (delta-147-148; K39X) mutant coding segmence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ54343;
in diphtheria vaccines. The risk of reversion to toxicity is much
                                portion of DF. The resulting muteins are not toxic, making them useful
                                                                                                                                                                                                                                                                                                                                                                                                                 toxicity and low risk of reversion, and derived toxoids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 · MAY - 1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1994 (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              780B, MAR44855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTGCTCTAATCTTTTCTGGTACC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1994-007178/01
                                                                                                                                                                                                                                                                                                                ; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consquative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-0901712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93WO-US04606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "wild type AAA (Lys) codon is replaced by
codon for any other amino acid or is absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product- diphtheria_toxin_mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312.,1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shote- "single chain translation product is readily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (*( ag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.0%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cleaved to form two sabadita (A and B), li
by a disalphide bond; wild type godons 147
(Val) and 148(Glu) have been deleted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Lys(39) codon is altered or deleted*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.2; DH 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.30+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ς,
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RESULT 15
AAQ54344/c
ID AAQ543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lower for the 147-148 double mutants than for the prior art 148 single mutant, while their immunogenicity is not impaired. The specification includes the wild type of coding sequence but does not include any mutant sequences, the wild type sequence was modified according to the description in the claims to give AAQ54343.
different amino acid residue. The third residue can be in the
            Oligonucleotide-directed mutagenesis of the wild-type diphtheria gene results in deletion of the codons for Val-147 and active site residue Glu-148, opt. a third residue which is essential for the full toxic activity of wild-type DT is deleted or altered to encode a
                                                                                      Claim 7; ; 42pp; English.
                                                                                                                   New DNA encoding diphtheria toxin deletion mutants - with no toxicity and low risk of reversion, and derived toxoids and transformed ceils, useful in vaccines
                                                                                                                                                                                                                                 Collier RJ. Killeen K.
                                                                                                                                                                                                                                                                                            18-JUN-1992;
                                                                                                                                                                                                                                                                                                                         17-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                     W09325210-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key Location/Qualifiers misc_difference 465..467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Df; protein exotoxin; NAD-dependent ADP-ribosyltransferase; vaccine diphtheria toxoid; deletion mutant, mutein; variant; double mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diphtheria toxin (delta-147-148; G52X) mutant coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 - JUN - 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ54344 standard; DNA; 1936 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1865 GTGATCTACTGTTTTCTGGTACC 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1936 BP; 571 A; 359 C; 470 G; 533 T; 3 other:
                                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                      23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reversion mutation; site-directed mutagenesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTGCTCTAATCTTTTCTGGTACC 23
                                                                                                                                                                                               1994-007178/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                    AAR44896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (tirst entry)
                                                                                                                                                                                                                                                                                          92US-0901712
                                                                                                                                                                                                                                                                                                                       93WO-US04606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag-_b
/product=_diphtheria_toxin_mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312..1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /noté- "wild-type GGG (Gly) codon is replaced by codon for any other amino acid or is absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.0%; Score 18.2;
87.0%; Fred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                           single chain translation product is readily cleaved to form two subunits (A and B), lind by a disulphide bond; wild-type codons 147 (Vai) and 148(Glu) have been deleted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ũ
                                                                                                                                                                                                                                                                                                                                                                                                                the Gly(52) codon is altered or deleted"
                                                                                                                                                                                                                               Mekalanes J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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  Matches
                                             Query Match
                                                                                                                                                               fragment A (see AAQ54341-7) or in the fragment B (see AAQ54348-054350) portion of DT. The resulting muleins are not toxic, making them useful in diphtherar vaccines. The risk of reversion to toxicity is much lower for the 147-148 double mutants than for the prior art 148 single mutant, while their immunogenicity is not impaired. The specification includes the wild-type DT coding sequence but does not include any mutant sequences; the wild-type sequence was modified according to
                                                                                             Sequence 1936 BF, 574 A, 359 C, 467 G, 533 T; 3 other;
                      Match 70.0%;
Local Similarity 87.0%;
                                                                                                                                           description in the claims to give AAQ54344.
     20:
  Conservative
0 ;
                         Score 18.2; DB 15;
Pred. No. 1.3e+02;
  Mismatches
                                             Length 1936;
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Search completed: January 14, 2003, 11:52:35 Job time: 7.29613 sees 밁

1865 GTGATCTACTGTTTTCTGGTACC 1843

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